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Comparative population genomics of crops and their wild relatives

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Rationale

Domestication strongly impacted phenotypic and genomic evolution in crop species. Understanding the genomic basis of the domestication process is thus a key to crop breeding and a unique opportunity to study rapid evolutionary processes on a short time scale.

Life-history and ecological traits may also influence genome evolution through their effect on key population genetic parameters (effective size, recombination rates, and mutation rates).

The aim of the project is to document **variation in genomic patterns** among a wide range of **crops** and **wild relative** species, during the domestication process and at a larger evolutionary scale.

Objectives

- Quantifying the evolution of diversity associated with domestication
- Identifying the genes involved in the domestication process
- Quantifying genome-wide selective patterns
- Investigating variations in domestication and genomic patterns associated with life history traits, domestication depth, or phylogenetic position.

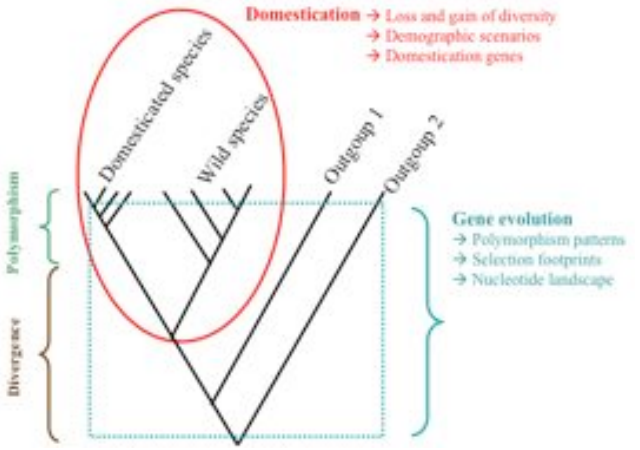

Figure 1: general design

Methodology

Sampling scheme

- Quadruplets of diploid species (Figure 1)
  - Focal crop species: 10 individuals
  - Wild relative: 10 individuals
  - Two outgroups: 1 individual each
- 11 quadruplets of species with contrasted life-history traits, across the angiosperm phylogeny (Table 1)

Sequencing

- Target: transcriptome (leaves+inflorescences+fruits)
- Combination of 454 (Roche) and Solexa (Illumina) technologies

Data analyses

- Data processing (assembly, SNP detection, orthology, functional annotation)
- Analyses of polymorphism and divergence patterns (Figure 1).

Table 1: list of studied species

Crop	Family	Cultivated taxon	Life span	Mating	Life form
African Rice	Poaceae	*Oryza glaberrima*	annual	self	herb
Banana	Musaceae	*Musa acuminata*	perennial	out	herb
Cocoa	Malvaceae	*Theobroma cacao*	perennial	mixed	tree
Coffea	Rubiaceae	*Coffea canephora*	perennial	out	tree
Einkorn wheat	Poaceae	*Triticum monococcum*	annual	self	herb
Grapevine	Vitaceae	*Vitis vinifera*	perennial	out	vine
Medicago	Fabaceae	*Medicago sativa*	perennial	out	herb
Palm	Arecaceae	*Elaeis guineensis*	perennial	out	"tree"
Pearl millet	Poaceae	*Pennisetum glaucum*	annual	out	herb
Sorghum	Poaceae	*Sorghum bicolor*	annual	self	herb
Tomato	Solanaceae	*Solanum lycopersicum*	annual	self	herb

The arcad project

This project is included in the **ARCAD project** (Agropolis Resource Center for Crop Conservation, Adaptation and Diversity), a flagship project funded by **Agropolis fundation**.

The ARCAD project aims at setting up a new open multi-function (**conservation, research & training**) platform devoted to the assessment and better use of **plant agrobiodiversity in Mediterranean and tropical regions**

It will focus on history and patterns of crop domestication and adaptation through evolutionary genomics, population genetics and social sciences studies.

Website: http://www.arcad-project.org/

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Expected outputs

- Fundamental knowledge on domestication process and genome evolution
- SNP discovery, identification of genes of interest, functional annotation
- Database in standardized format, pipeline development for genome wide analyses

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